

FIG. 1A

1 AAGCTTTCTTGGCCCCCTAACAGCAACCACATTATACTCTTACTGGCTATTCCTTGGCCTT 60
61 CAATACCCAGCCCAGGGGACCCCTCTTCCAGGGAGCCCCGCTTGTACTCCTGAGATGTCA 120
121 TGTCTTCTTGCAGAGCTCTTCCCTACGGCATCGGGACGGCGGTTACCCCTTTTGCCTCT 180
181 CCGGATAAACTGTAAGCTACTTGAGAGCAGAGAACATCCATTGTTTCGCTGTGGCATCCGT 240
241 GGTACCTAGCACGGCATCTGACATATTATCAGATCTTCCACAAAGGCCAGTTTACGGTTG 300
301 AATGCCCCGTGAATTTCAGGCTCCAGTGGGAGAGCGAGGAAGTAATAAAGCCGGTGATAA 360
361 ATGCCGCCGTGGAGACACCAGCGGGCTGCCGTGAGACTAATGGAGAGGACAGTAACGTTA 420
421 TCTCTAATGCGAGGGTGGTTATAGAGTACATTTTCATAACACCTTTAAAGCTCTTTACAC 480
481 GCATTATCCAATTTGATCCTCATAAAAGCCTGGAGATGTGTATATTGTGGTGGATGGAGG 540
541 GGGAGTCTTTAGCAGTTATGGGATATGCCTGAAGTCGTGCAGCTAGTAAATGGCTGGATT 600
601 CAAACCAGACCTCAAAAGCCTGCCTGTTTGTCTCATGCCCCCTGCCCCGACTGCCCACTCT 660
661 GTGGCCACAGCACAACCTACCGTCGCTTTCTTGATCCGTTTCTTGATCCGGCTGTGCT 720
721 CTCCCCAAGGAATGCTTTTCATTAACATATGTCTAGGTAATGAATTATCTTGACTCTGAG 780
781 GAGGCCATAGCACATGCCGTAACGCGACAGCTCCTTTGATCTGCATCTGAGGCTGTGGCT 840
841 GGTAACGGGCGTGGGGAGGGGGCGTTTCGCTGAGACCCAGGGACACGCCATGTGTGGTTC 900
901 CCTCTGTTTCCAGGCCCCAGAAGCACATCCCGGAAAGGAAAATGCGCTGTGGACCCCTGT 960
M R C G P L C
961 GCCGATTCTGCTGGCTTTGGCCTATCTGTCTACGTTGAAGCCGTGCCCATCTGGAGAG 1020
R F L L A L A Y L S Y V E A V P I W R V
1021 TCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCAACAGGATCAGTGACATTTAC 1080
Q D D T K T L I K T I V T R I S D I S H
1081 ACATGGTAGGGAAGGCCTGGGAGACAAGGTGCAACCTGTGGCCAGCCCSGGGGAGGAGG 1140
M
1141 GGTACCGGACCTCAGAGGTTGGCGGAGGTGGGAAGGGTCGGCGGTGGCCTTGACGCCTCC 1200
1201 CCCACCCCCCAACCAGCTGCCTTTGCTCCTCCGCTTCCCTCACCACACCCCCCACGT 1260
1261 CCTTATCCTCCTTCTTCCCAGACTGGAATCCTGATGCCCAGGACTAGAGGAAGCCCTAAA 1320
1321 GGTCTGTGTGCCTTTGCCAGGTGCGCAGACCCCCAGCATCATCCCCTCTGGCCTCCAT 1380
1381 CACGTCTCCGGAATGTTCTAATCTGTAGGAATTCTTCTGGTGACAGCTGAACCTCTGACC 1440
1441 CTGCGGACGCCCCCTTACTGCTAGTCTGCCCATTGAGCCTTTTTTCTTATACAACCCTCT 1500
1501 ACATGTTTGCAAACCTCTCTCAATGTCCCCAGGGTGTTTTCTCTGGGGTCCGCAGGCCGA 1560
1561 GACCTTCAGCCTCTTCTCAGCTGAGGTCCGTCTTTAGAAATCAGAAGACGAGGTGTGACT 1620
1621 CCTCACCTGCTGTTCCCTCTCTGTAAAATCTCAAGCACGTTAAGTCCCTCCGTGTCTGA 1680
1681 AACCTTAGTTTCCCTCATCCAGATAATGGGACTGTTACTGGGAAGATGTTACCGGAATCC 1740
1741 AGGGTCTTGCCTCATGGAGCTCAAGAATGAACTTGGCGAAGCACAGGGAGCCGAGCAAG 1800

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FIG. 1B

1801	CAGAAGTCTTTATTACAGGAAGGCAGACAGCTCCCAGCACAGACACGGGGAGGGAAAGAGT	1860
1861	CCCCCGCCCATTTGTTCTACGGAGGTTTTTATCACTTAAAGACGGGAGTACCAATGTGGG	1920
1921	GTCCAGATATCCGTTCTTCTTCCCATTGCCAGTTTACCTATATGGCGCCTTGTCAGGA	1980
1981	GGGACTCTGTAGAGTTAGGGGTGCTCCGTAAGTTTTATGGTGCGTCTGCTCTTCTCTGCC	2040
2041	CTAGACTTAGAGTCGCCACTCTTTCATTCTTCTGCTCACAGTCAAATGCATAGGTCAGG	2100
2101	GGTTAATTCCCACCTTCACAGAAATCAAATGTCCTTTCAATAGTTAATCTTCCAATAAGC	2160
2161	AAGGCCTGCTTGTCTTGATTAGTTTTTACAAATCTTAAACCATGGCCATTAATCAGGGAA	2220
2221	GAGATCGAAGCCCATGTTCCCACTAACTGCCTGAATTATTAGTCTGCCTCAGGACTAT	2280
2281	CTTAATAGTCTTCGCAAGGTTGTTTTGAGATTAAATTAGATAGGAGTTCCTGTCGAGGCG	2340
2341	CGACGGAAACAGATCCGACTCAGAACCATGAGACAGGTTGATCCCTGGCTTTGTCAGTG	2400
2401	GGTTAGGATCTGGTGCTGCTGTGAGCTGTGGTGTAGGTCGCAGAGGTGGCTCGGATCCCCG	2460
2461	CGTTGCTGTGGCTGTGGTGTAGGCCGGTGACAGAGCTCCGATTAGACCCCTAGCCTGGG	2520
2521	AACCTCCATGTGCCGCGGGTACCGCTAAAAAAGACAAAAGATGGAAAAAAAAGGTTA	2580
2581	CATTAGATAAAGCAAGTGACTCCTCCACCACCACACATATCCCTGCAGAACCCAGGACAGA	2640
2641	GCATGCCTTCTTGAAAAGTTTTCGGTTGTGGCTTTGATAGCACCCAGCCTTAAAAGCCAG	2700
2701	CTTTTCAATCTGCCCAGAGCAGTCTGGAGACTTCCGCATCTCCTGGCCACTCTGAGTTTC	2760
2761	TAACAGTGGCCTTGCGGAGCCTGGGAGCAGTCCGGTGGCCAGAAGCAGGGACAGCTGAGA	2820
2821	ACCAGATAGAGTCTTGGCACTTTCAAGAGAAAACCCTAAGTCTCCTTCTTCCAGCCATGC	2880
2881	AACAGCTGCGCATGACAGATCCAGCGTGTCCCAGCCTGTGTGGTGCAGGGAGTGAYGCTG	2940
2941	CGNNYAGGGYGYGGGGGAGCTGAGGAGCGAGGCGGGGCATCGNNGGGCTGCAGCCTCCAT	3000
3001	CCCTAAGTGGGGAGACTTCATGAAGAGCCTGACCAGNAGGGAGGGGCATGTGTGGAGGAC	3060
3061	CTCAGGGCCTGGGGAAGGCTAGACCCAACCTATGTGAGAAACAGACAGTCGTGGCTGGTTC	3120
3121	TACAGAAGAGGCATCTGGAGGCCATTGCAATGCCCAAAGCTGTCTGGGTGAGGCAGGGCT	3180
3181	TGCTAGGCAGAAGACAGAAGGCCGTGAGACCAGCTTGGAGGCTTGGCAGCCACGCCAGCC	3240
3241	CAAGGAGTTCTGGGCCTAGATAGGATTGTGTGGAAGGGGAAGAGGCAGCCGGAGGTGGGGG	3300
3301	GTGGGGGTGGACCCGTCTCCACGCCTGCAGGAAGGCCAGGGGCTGCAGAGCCAACATCTC	3360
3361	TCTCGCTGAGCGTCTCGCTCTCCCTTCTCCTGCACAGCAGTCTGTCTCCTCCAAACAG	3420
	Q S V S S K Q	
3421	AGGGTCACCGGTTTGGACTTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATG	3480
	R V T G L D F I P G L H P V L S L S K M	
3481	GACCAGACCCTGGCGATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATC	3540
	D Q T L A I Y Q Q I L T S L P S R N V I	
3541	CAAATATCGAATGACCTGGAGAACCTCCGGACCTTCTCCACCTGCTGGCCTCCTCCAAG	3600
	Q I S N D L E N L R D L L H L L A S S K	
3601	AGCTGCCCCCTTGCCAGCAGGGCCTGGAGACCTTGAGAGCCTGGGCGGCGTCTGGAA	3660
	S C P L P S R A L E T L E S L G G V L E	

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FIG. 1C

3661	GCCTCCCTCTACTCCACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGAC	3720
	A S L Y S T E V V A L S R L Q G A L Q D	
3721	ATGCTGCGGCAGCTGGACCTCAGCCCTGGCTGCTGAAGCCTTGAAGGCCTCTCTCCCCAC	3780
	M L R Q L D L S P G C *	
3781	AGTCGGGGGAAGAAACCTGAGCTTCCAGGAGTCTGCTGGAGAAGAGAGCCTGTGCGGACC	3840
3841	TCCTCTCTGCAGGTCTGCGGACCATTCTCTCTCGCTCCGCTAAGCTGCTCTTCCAAAGG	3900
3901	CAGAAACTCCAAGGCACGACACCAAAGACAGAAAGGCCTGGTTCCGCGCCACCGGAAA	3960
3961	GGGGGCGCCGTCCAGCCAACGGTGGACTAGATTTTCGATTTTCCACCAACGTCTTCCTTC	4020
4021	CTGTTCCATCTCCAGCTCACCGCGTGCTTCAGCGTGACCGGGGGGATTTAGAGCCTTTC	4080
4081	GACCATCAAGCAGGGTTCATCTGAGAATTCGGGGAGCACGGTGAAGGCTACAGGCACA	4140
4141	CACAGCTGGATGCTCCACGCAACACAAGTTGGAAGCATTCTTTATTTATTATGCGGTG	4200
4201	TATTCTGGTTGGATTGAAGCAAAACACCAGCCTTTCAGGCTCTCTGGGGTCAGCCGGG	4260
4261	GCTAGGGGGAGGCTCCCCAGGTGCTGTTTCCAGTACCATCCATGGGCCTGCTGAGGCCAA	4320
4321	CCCATTTTGAGTGACTTGAGGGCTCTCAAGGTCGTTCTCTAGAGACTGGCTTTGTTTCTA	4380
4381	CTGTGACTGACTTTAAAACTGCAGCGTGTGACTGGCATCGCCTGCGCGGATCTCGAAGG	4440
4441	GCCAGGTTCTCTTAGAAAGAAGAAGATGAACCTTTGTCAGGGGTGTGTACGCGGAGACAGG	4500
4501	AAGTGTGTTGGTGGGCGGGGCATGGATCCAGAATGTGTATTTCTTGTGTGATGGACATTT	4560
4561	GTGTGAGGGGCTCTCTGGACAGGGTGAGGTCATTGTCTCATCTTCGTGGTTTTTCATGAGA	4620
4621	GAAGGAGATGATTCCCTTCACGGGGGTCGTGGGGTTTTTGCCAGCCGCCCGTGCAGGAGTGG	4680
4681	GGAAGGGGCTGAAGCCGAAGACCGTTGGGGGCCGTGGTGAGCTCTGCCTTCTCCAGCTGC	4740
4741	TAGAGGCTGGTCTTCTCATCAGGGAGTGAGGCTCTCGCGTTGGAGACAGTGATCCCCAG	4800
4801	GGCGGGATCCTTGCCGTGGCCCTCTGAATGGTCTGGGTGATCCACACTGATGTCATAAC	4860
4861	AGGGAAGTGCCCTGGTTTGGGATTTGTATGCTCACCCAAAGCAAGGGCCTGCTTCCCATC	4920
4921	CATTTTGGGAAGGATTTTTTCTCCAGGGGGAGGGTGAAAGCTCTGGGAGGTCTGTGGGCT	4980
4981	TACGAGATGGTCCAAGTCTTGGGTGAGTGAGTCCCGGACTCGTGACCGCCTCGAGGAGC	5040
5041	CCCCTTCTCCCTACAGGTCATGTTCAATAGGTCAAACAAGGAGGCATGGGTTTCCACCAT	5100
5101	CCTGCCGCTGTGATGCAGCCATCGCACTACAGGAGGTAGATCTGTCCAAGGAAATTTGAA	5160
5161	TCTCAAGCAATCACTTTCAAGACTGAGCATCTATTGTGCTCAGCCCCAACTGGTGCTATG	5220
5221	GGCTCAGAGAAGCTCATCAAATAAATATTAATAATCCAGTCTTGCCTTCAGGACCTTGCAT	5280
5281	TCCAGATGATAACACCTCCCCACACCCCGTCTGCAGAGGCTGTCAATTCACCATGGCAA	5340
5341	CCGAGCAGCTGAAACACAGTGCGGTCTCAGCAGGTGGAAAGGCTGAGCTGAGGAGGGCA	5400
5401	GTGCCCCGGGCCACAGGCTAACCTGCTTGCACTTGGTAGCATTTTACTGTTTCGGGGCG	5460
5461	CATCAGCATCTATTACTGAGAAGCCGCATCCCTTTGAAGCAGGATAGCTGAGACTATAAA	5520
5521	AATAAGAAAATACCAGAGTTCCCTTGTGGCACAGAGGGCTAAGGATCCAGTGTGTTGCT	5580
5581	GCAGCAGCTTGGGTACGGCTGTGGCAAGGGTTCGATCCCTGGCCTGGGAACTTTACAT	5640

FIG. 1D

5641 GTTGCAGGCAAGGCCAAAAAATAAATAAATAAAAAATAAACAAAAAAAAACAAGACCA 5700
5701 TAACAGCAGACTGGTGGCAAACCAGGACTAGAACCTGGGTCCTCTGACCCCTAGAGTCAG 5760
5761 TGTCCCCTGAGCCAGCTAGTGTCTCTGGGGACGGGAACAGGGTTGGGCAGGGAGTTCAG 5820
5821 GAAGTGTCTGCTGGAAGAGCGGAGTTTCCAGGCTGATTTTGCAGGAGGTGAGGGAAGTGG 5880
5881 ATTGCCTGGAGGGAGGAGGCTGTTTTGTTTGAAGCTT 5917

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[illegible]

Size	501 , Select	1	
1	ATGCGCTGTGGACCCCTGTGCCGATTCCTGCTGGCTTTGGCCTATCTGTCCTACGTTGAA	60	
1	M R C G P L C R F L L A L A Y L S Y V E	20	
61	GCCGTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACC	120	
21	A V P I W R V Q D D T K T L I K T I V T	40	
121	AGGATCAGTGACATTTACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTG	180	
41	R I S D I S H M Q S V S S K Q R V T G L	60	
181	GACTTCATCCCTGGGCTCCATCCTGTCTCTGAGTTTGTCCAAGATGGACCAGACCCTGGCG	240	
61	D F I P G L H P V L S L S K M D Q T L A	80	
241	ATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGAC	300	
81	I Y Q Q I L T S L P S R N V I Q I S N D	100	
301	CTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCCTTGCCC	360	
101	L E N L R D L L H L L A S S K S C P L P	120	
361	AGCAGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCTGGAAGCCTCCCTCTACTCC	420	
121	S R A L E T L E S L G G V L E A S L Y S	140	
421	ACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCAGCTG	480	
141	T E V V A L S R L Q G A L Q D M L R Q L	160	
481	GACCTCAGCCCTGGCTGCTGA	501	
161	D L S P G C *	167	

FIG. 3

1	GTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGG	60
1	V P I W R V Q D D T K T L I K T I V T R	20
61	ATCAGTGACATTTTACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTGGAC	120
21	I S D I S H M Q S V S S K Q R V T G L D	40
121	TTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCGATC	180
41	F I P G L H P V L S L S K M D Q T L A I	60
181	TACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGACCTG	240
61	Y Q Q I L T S L P S R N V I Q I S N D L	80
241	GAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCTTGCCCAGC	300
81	E N L R D L L H L L A S S K S C P L P S	100
301	AGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCCTGGAAGCCTCCCTCTACTCCACG	360
101	R A L E T L E S L G G V L E A S L Y S T	120
361	GAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCACGTGGAC	420
121	E V V A L S R L Q G A L Q D M L R H V D	140
421	CTCAGCCCTGGCTGC	435
141	L S P G C	145

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FIG. 4

		10	20	30	40	50	
PIG	1	ATGCCCTGTG	GACCCCTGTG	CCGATTCCTG	CTGGCTTTGG	CC-TATCTGT	50
HUMAN	1	ATGCATTTGG	GAACCCCTGTG	CCGATTCCTG	-TGGCTTTGG	CCCTATCTTT	50
MOUSE	1	ATGTGCTGGA	GACCCCTGTG	TCCGTTTCCTG	-TGGCTTTGG	TCCCTATCTGT	50
		60	70	80	90	100	
PIG	51	CCTACGTTGG	AGCCGTGCCC	ATCTGGGCGG	TCCAGGATGA	CACCAAAACC	100
HUMAN	51	TCTATGTCGA	AGCTGTGCCC	ATCCAAAGAG	TCCAGATGA	CACCAAAACC	100
MOUSE	51	CTTATGTTCA	AGCAGTGCCG	ATCCAGAAAG	TCCAGGATGA	CACCAAAACC	100
		110	120	130	140	150	
PIG	101	CTCATCAAGA	CCATTGTCAC	CAGGATCGGT	GACATTTTAC	ACATGCACTC	150
HUMAN	101	CTCATCAAGA	CAATTGTCAC	CAGGATCGAT	GACATTTTAC	ACACGCAGTC	150
MOUSE	101	CTCATCAAGA	CCATTGTCAC	CAGGATCGAT	GACATTTTAC	ACACGCAGTC	150
		160	170	180	190	200	
PIG	151	TGTCTCCTCC	AAACAGAGGG	TCACCGGTTT	GGACTTCATT	CCTGGGGCTCC	200
HUMAN	151	AGTCTCCTCC	AAACAGAAAG	TCACCGGTTT	GGACTTCATT	CCTGGGGCTCC	200
MOUSE	151	GCTATCCGCC	AAACAGAGGG	TCACTGGCTT	GGACTTCATT	CCTGGGGCTTC	200
		210	220	230	240	250	
PIG	201	ATCCGTGTCCT	GAGTTTGTCC	AAGATGGACC	AGACCTTGGC	GATCTACCAA	250
HUMAN	201	ACCCCATCCCT	GACCTTATCC	AAGATGGACC	AGACCTTGGC	AGTCTACCAA	250
MOUSE	201	ACCCCATTCCT	GAGTTTGTCC	AAGATGGACC	AGACTCTGGC	AGTCTATCAA	250
		260	270	280	290	300	
PIG	251	CAGATCCTCA	CCAGTCTGCC	TTCCAGAAAT	GTGATCCAA	TATCCAAATGA	300
HUMAN	251	CAGATCCTCA	CCAGTATGCC	TTCCAGAAAC	GTGATCCAA	TATCCAAACGA	300
MOUSE	251	CAGATCCTCA	CCAGCTTGCC	TTCCCAAAAT	GTGCTCCAGA	TATCCCAATGA	300
		310	320	330	340	350	
PIG	301	CCTGGAGAAC	CTCCGGGACC	TTCTCCACCT	GCTGGCCTCC	TCCAAGAGCT	350
HUMAN	301	CCTGGAGAAC	CTCCGGGATC	TTCTTCACGT	GCTGGCCTTC	TCTAAGAGCT	350
MOUSE	301	CCTGGAGAAAT	CTCCGAGACC	TCCTCCATCT	GCTGGCCTTC	TCCAAGAGCT	350
		360	370	380	390	400	
PIG	351	GGCCCTTTGCC	CAG---CAGG	GCCTGGAGA	CCTTGGAGAG	CCTGGGCGGC	400
HUMAN	351	GGCACTTTGCC	CTGGGCCAGT	GGCCTGGAGA	CCTTGGACAG	CCTGGGGGGT	400
MOUSE	351	GCTCCCTTGCC	TCAGACCACT	GGCCTGCAGA	AGCCAGAGAG	CCTGGATGGC	400
		410	420	430	440	450	
PIG	401	GTCTCTGGAAG	CCTCCTCTTA	CTCCACGGAG	GTGGTGGCCC	TGAGCAGGCT	450
HUMAN	401	GTCTCTGGAAG	CTCTCAGGCTA	CTCCACAGAG	GTGGTGGCCC	TGAGCAGGCT	450
MOUSE	401	GTCTCTGGAAG	CCTCACTCTA	CTCCACAGAG	GTGGTGGCTT	TGAGCAGGCT	450
		460	470	480	490	500	
PIG	451	GCAGGGGGCT	CTGCAGGACA	TGCTGCGGCA	GCTGGACCTC	AGCCCTGGCT	500
HUMAN	451	GCAGGGGGTCT	CTGCAGGACA	TGCTGTGGCA	GCTGGACCTC	AGCCCTGGCT	500
MOUSE	451	GCAGGGCTCT	CTGCAGGACA	TTCTTCAACA	GTGGATGTTT	AGCCCTGAAT	500
		510	520	530	540	550	
PIG	501	GCTGA	550
HUMAN	501	GCTGA	550
MOUSE	501	GCTGA	550

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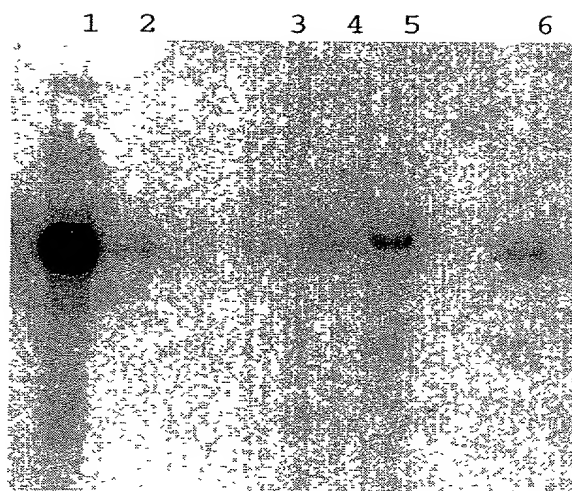


FIG. 5

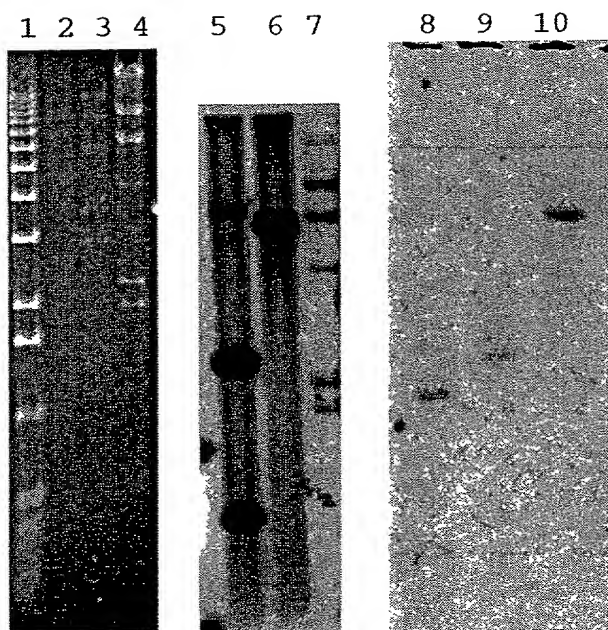


FIG. 6

1 2 3 4 5 6

97.4
68
43
29
18.4
14.3

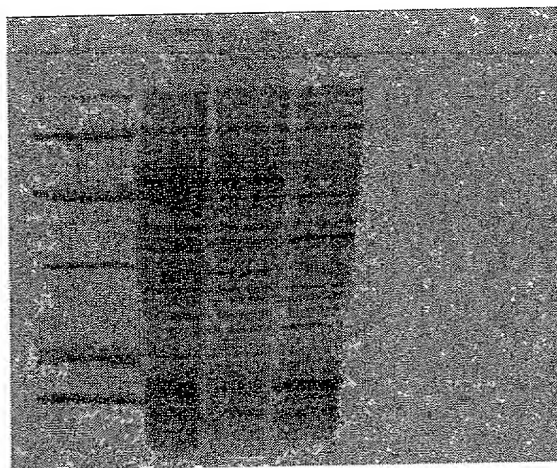


FIG. 7

FIG. 8

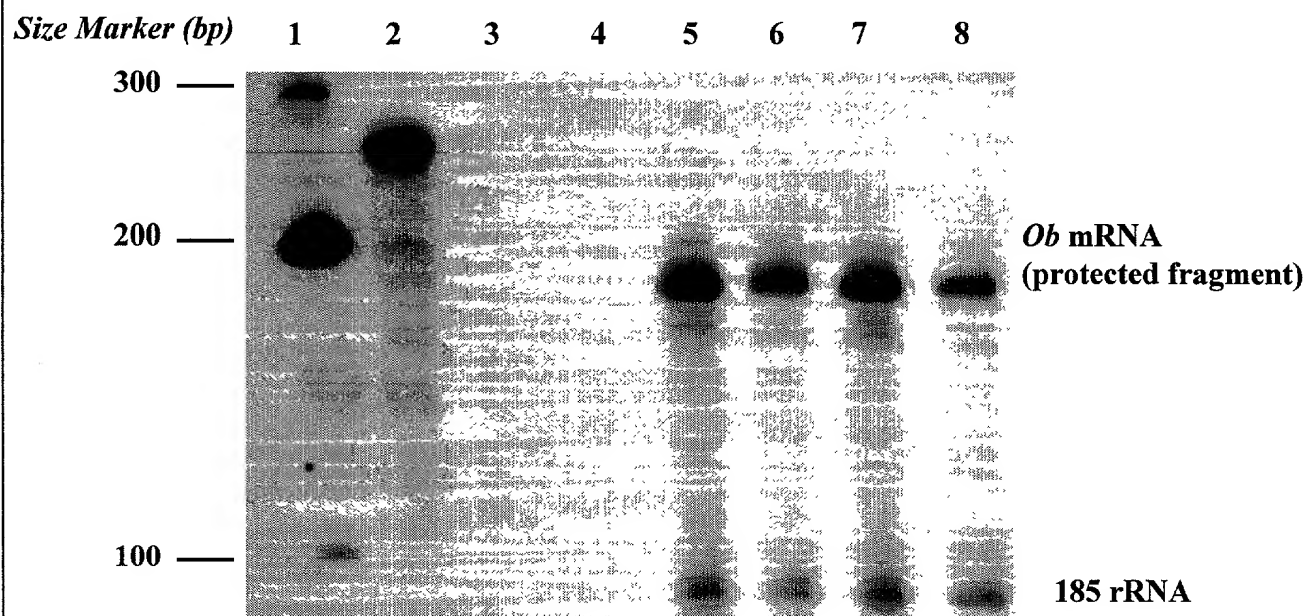


FIG. 9

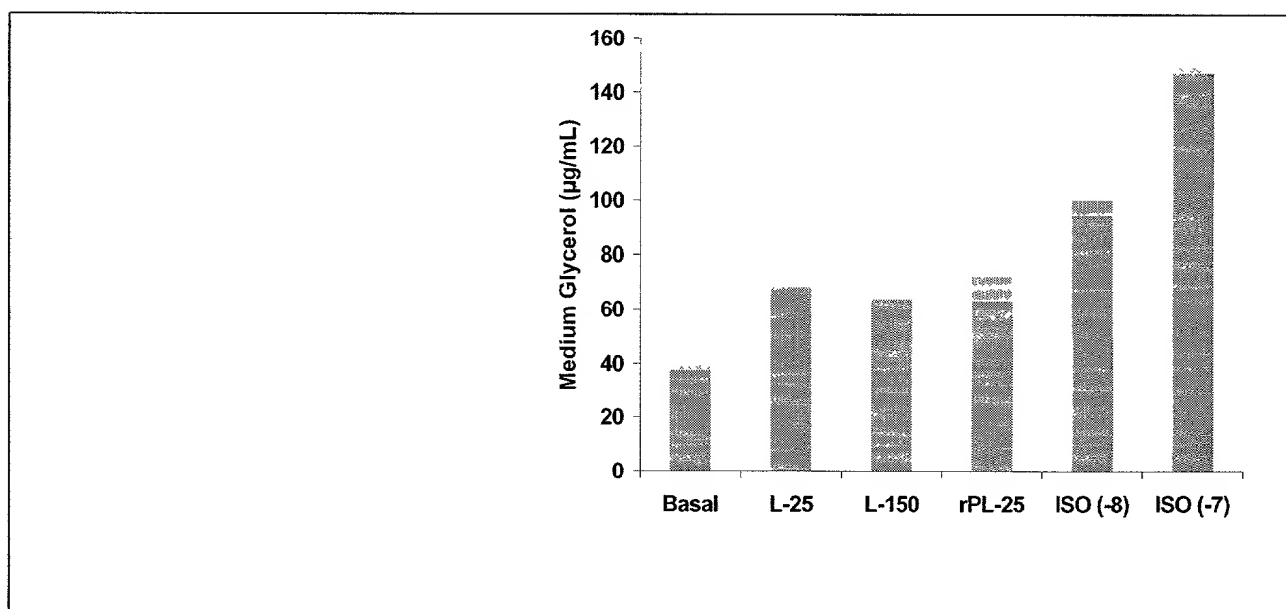


FIG. 10

Western blot of recombinant human and porcine leptin with the polyclonal antibody to synthetic peptide based on the C-terminal sequence of porcine leptin.

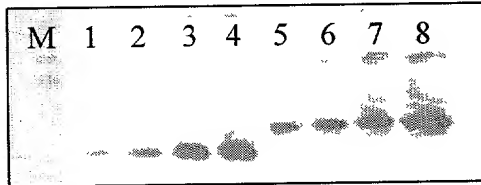


FIG. 11

A polyclonal antibody to recombinant porcine leptin immunoprecipitates leptin from pig serum, cerebral spinal fluid (CSF), and adipose extracts.

